



CASE 4-31612A

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF

Art Unit: 1632

COHEN ET AL.

Examiner: Valarie E. Bertoglio

APPLICATION NO: 09/964,899

FILED: SEPTEMBER 27, 2001

FOR: IDENTIFICATION OF GENES INVOLVED IN ALZHEIMER'S
DISEASE USING DROSOPHILIA MELANOGASTER

Commissioner for Patents
P. O. Box 1450
Alexandria, VA 22313-1450

RESPONSE TO RESTRICTION REQUIREMENT

Sir:

In the Office Action dated October 3, 2003, restriction was required between the following groups of claims:

- I. Claims 1-3 and 27-30, drawn to a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the Abeta portion of human APP wherein said DNA sequence encodes Abeta40 (SEQ ID NO: 1) and methods of using the fly to identify compounds useful for treatment, classified in class 800;800, subclass 3;13.
- II. Claims 1-3 and 27-30, drawn to a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the Abeta portion of human APP wherein said DNA sequence encodes Abeta42 (SEQ ID NO:2) and methods of using the fly to identify compounds useful for treatment, classified in class 800;800, subclass 3;13.

- III. Claims 4-8 and 31-36, drawn to a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the wild type C99 portion of human APP (SEQ ID NO:3) and methods using the fly to identify compounds useful for treatment, classified in class 800;800, subclass 3;13.
- IV. Claims 4-8 and 31-36, drawn to a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the C99 portion of human APP with the London mutation (SEQ ID NO:4) and methods using the fly to identify compounds useful for treatment, classified in class 800;800, subclass 3;13.
- V. Claims 9-12, drawn to a method of identifying genetic modifiers using a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the Abeta portion of human APP wherein said DNA sequence encodes Abeta40 (SEQ ID NO:1), classified in class 800, subclass 3.
- VI. Claims 9-12, drawn to a method of identifying genetic modifiers using a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the Abeta portion of human APP wherein said DNA sequence encodes Abeta42 (SEQ ID NO:2), classified in class 800, subclass 3.
- VII. Claims 13-18, drawn to a method of identifying genetic modifiers using a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the wild type C99 portion of human APP (SEQ ID NO:3), classified in class 800, subclass 3.
- VIII. Claims 13-18, drawn to a method of identifying genetic modifiers using a transgenic fly whose genome comprises a DNA Sequence encoding a polypeptide comprising the C99 portion of human APP with the London mutation (SEQ ID NO:4), classified in class 800, subclass 3.
- IX. Claims 19-21, drawn to a method of identifying targets for therapeutics, comprising identifying human homologs of genetic modifiers identified using a transgenic fly comprising the Abeta portion of human APP, classified in class 702, subclass 19.

- X. Claims 22-24, drawn to a method of identifying targets for therapeutics, comprising identifying human homologs of genetic modifiers identified using a transgenic fly comprising a DNA Sequence encoding a polypeptide comprising the C99 portion of human APP, classified in class 702, subclass 19.
- XI. Claims 25 and 26, drawn to a method of identifying therapeutic targets comprising identifying genes involved in specific molecular pathways, unclassifiable.
- XII. Claim 37, drawn to a method for identifying treatment compounds using a model of Alzheimer's Disease comprising assaying for changes in a homolog of a genetic modifier identified using a transgenic fly comprising the Abeta portion of human APP, classified in class 435;800, subclass 4;3.
- XIII. Claim 38, drawn to a method for identifying treatment compounds using a model of Alzheimer's Disease comprising assaying for changes in a homolog of a genetic modifier identified using a transgenic fly comprising the C99 portion of human APP, classified in class 435;800, subclass 4;3.
- XIV. Claims 39 and 40, drawn to a method for identifying treatment compounds using a model of Alzheimer's Disease comprising assaying for changes in a homolog of a genetic modifier disclosed in Table 1 classified in class 435;800, subclass 4;3.
- XV. Claims 41-44, 54-57 and 68-71 drawn to a method of treating conditions associated with abnormal regulation of the APP pathway using a modulator of a human homolog of a genetic modifier identified using a transgenic fly comprising the Abeta portion of human APP and a pharmaceutical comprising the modulator, classified in class 514;530;530, subclass 2;300;350.
- XVI. Claims 45-48, 58-61 and 72-75, drawn to a method of treating conditions associated with abnormal regulation of the APP pathway using a modulator of a human homolog of a genetic modifier identified using a transgenic fly comprising the C99 portion of human APP and a pharmaceutical comprising the modulator, classified in class 514;530;530, subclass 2;300;350.

- XVII. Claims 49-53, 62-67 and 76-81 drawn to a method of treating conditions associated with abnormal regulation of the APP pathway using a modulator of a human homolog of a genetic modifier disclosed in Table 1 and a pharmaceutical comprising the modulator, classified in class 514;530;530, subclass 2;300;350.
- XVIII. Claims 82, 83 and 90, drawn to a method of treating conditions associated with abnormal regulation of the APP pathway comprising assaying mRNA and/or protein levels of a genetic modifier identified using a transgenic fly comprising the Abeta portion of human APP and administering a substance to treat said condition, classified in class 514;530;530, subclass 2;300;350.
- XIX. Claims 84, 85 and 91, drawn to a method of treating conditions associated with abnormal regulation of the APP pathway comprising assaying mRNA and/or protein levels of a genetic modifier identified using a transgenic fly comprising the C99 portion of human APP and administering a substance to treat said condition, classified in class 514;530;530, subclass 2;300;350.
- XX. Claims 84, 85, 92 and 93, drawn to a method of treating conditions associated with abnormal regulation of the APP pathway comprising assaying mRNA and/or protein levels of a genetic modifier listed in Table 1 and administering a substance to treat said condition, classified in class 514;530;530, subclass 2;300;350.
- XXI. Claims 94 and 95, drawn to a method of diagnosis comprising measuring mRNA or polypeptides encoded by a genetic modifier identified using a transgenic fly comprising the Abeta portion of human APP, classified in class 435;435, subclass 6;7.14.
- XXII. Claims 96 and 97, drawn to a method of diagnosis comprising measuring mRNA or polypeptides encoded by a genetic modifier identified using a transgenic fly comprising the C99 portion of human APP, classified in class 435;435, subclass 6;7.14.
- XXIII. Claims 98-101, drawn to a method of diagnosis comprising measuring mRNA or polypeptides encoded by a genetic modifier listed in Table 1, classified in class 435;435, subclass 6;7.14.

XXIV. Claims 102 and 103, drawn to a gene therapy method of treating conditions associated with abnormal regulation of the APP pathway comprising introducing nucleic acids encoding a genetic modifier identified using a transgenic fly comprising the Abeta portion of human APP, classified in class 514, subclass 44.

XXV. Claims 104 and 105, drawn to a gene therapy method of treating conditions associated with abnormal regulation of the APP pathway comprising introducing nucleic acids encoding a genetic modifier identified using a transgenic fly comprising the C99 portion of human APP, classified in class 514, subclass 44.

XXVI. Claims 106-109, drawn to a gene therapy method of treating conditions associated with abnormal regulation of the APP pathway comprising introducing nucleic acids encoding a genetic modifier listed in Table 1, classified in class 514, subclass 44.

In response to the restriction requirement of record, applicants hereby elect Group II, claims 1-3 and 27-30 with traverse.

Applicants respectfully disagree with the Examiner's restriction of Group I (Ab40 or Seq ID No. 1) from Group II (Ab42 or Seq ID No. 2). Applicants submit that the inventions claimed in claims 1-3 and 27-30 restricted to Seq ID No. 1 (Group I) and claims 1-3 and 27-30 restricted to Seq ID No. 2 (Group II) amount to combination and subcombination inventions, respectively, and are therefore not patentably distinct.

MPEP § 806.05(c) sets forth the criteria for distinctness for combinations and subcombinations. In order to establish that combination and subcombination inventions are distinct, two-way distinctness must be demonstrated. The inventions are distinct if it can be shown that a combination as claimed:

- (A) does not require the particulars of the subcombination as claimed for patentability (to show novelty and unobviousness), and
- (B) the subcombination can be shown to have utility either by itself or in other and different relations.

When these factors cannot be shown, such inventions are not distinct.

Here, criterion (A) is not met, because the subcombination of Group II as claimed (transgenic fly comprising Abeta42, Seq ID. No. 2) does require the particulars of the combination of Group I (transgenic fly comprising Abeta40, Seq ID. No. 1) for patentability over the art. The DNA sequence encoding AB40 (Seq ID 1) is homologous over 123 nucleic acid bases with the DNA sequence encoding AB42 (Seq ID 2) and differs by 6 contiguous nucleotides (total 129 bases). Thus, the AB of the invention are clearly related as species and are not independent. If Seq ID No. 1 is patentable over the prior art, then so is Seq ID No. 2 comprising the homologous regions of Seq ID No. 1.

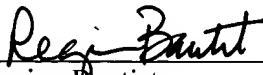
Furthermore, MPEP § 803 states: "If the search and examination of an entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent or distinct inventions." Here, the recited SEQ ID NOs of inventions I and II are not patentably distinct as discussed above and a search for one sequence would encompass a search for the other sequence as the claimed sequences merely differ in 6 contiguous nucleic acid base pairs. Thus, the examiner's statement on pages 7 of the restriction/election requirement that "the burden required to search any of inventions I-IV together would be undue" is untenable.

Accordingly, Applicant respectfully requests that the claims in Group I and II be consolidated with the provisionally elected claims in Group II and examined together as a combination/subcombination.

No new matter has been added. If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is invited to call the undersigned attorney.

An early and favorable action on the merits is respectfully requested.

Respectfully submitted,



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